

Patent Application US/07/666,252

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: WAHL, DR, GEOFFREY M
O'GORMAN DR, STEPHEN V

(ii) TITLE OF INVENTION: FLP-MEDIATED GENE MODIFICATION IN
MAMMALIAN CELLS, AND COMPOSITIONS AND CELLS USEFUL
THEREFOR

(iii) NUMBER OF SEQUENCES: 2

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: FITCH, EVEN, TABIN & FLANNERY
(B) STREET: 135 South LaSalle Street, Suite 900
(C) CITY: Chicago
(D) STATE: Illinois
(E) COUNTRY: USA
(F) ZIP: 60603

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/666,252
(B) FILING DATE: 08-MAR-1991
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: REITER MR, STEPHEN E
(B) REGISTRATION NUMBER: 31192
(C) REFERENCE/DOCKET NUMBER: 50730

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (619) 552-1311
(B) TELEFAX: (619) 552-0095
(C) TELEX: 20 6566 PATLAW CGO

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1380 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

Patent Application US/07/666,252

54
55
56 (vii) IMMEDIATE SOURCE:
57 (B) CLONE: NATIVE FLP
58
59 (ix) FEATURE:
60 (A) NAME/KEY: CDS
61 (B) LOCATION: 1..1269
62
63
64 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
65
66 ATG CCA CAA TTT GAT ATA TTA TGT AAA ACA CCA CCT AAG GTG CTT GTT 48
67 Met Pro Gln Phe Asp Ile Leu Cys Lys Thr Pro Pro Lys Val Leu Val
68 1 5 10 15
69
70 CGT CAG TTT GTG GAA AGG TTT GAA AGA CCT TCA GGT GAG AAA ATA GCA 96
71 Arg Gln Phe Val Glu Arg Phe Glu Arg Pro Ser Gly Glu Lys Ile Ala
72 20 25 30
73
74 TTA TGT GCT GCT GAA CTA ACC TAT TTA TGT TGG ATG ATT ACA CAT AAC 144
75 Leu Cys Ala Ala Glu Leu Thr Tyr Leu Cys Trp Met Ile Thr His Asn
76 35 40 45
77
78 GGA ACA GCA ATC AAG AGA GCC ACA TTC ATG AGC TAT AAT ACT ATC ATA 192
79 Gly Thr Ala Ile Lys Arg Ala Thr Phe Met Ser Tyr Asn Thr Ile Ile
80 50 55 60
81
82 AGC AAT TCG CTG AGT TTC GAT ATT GTC AAT AAA TCA CTC CAG TTT AAA 240
83 Ser Asn Ser Leu Ser Phe Asp Ile Val Asn Lys Ser Leu Gln Phe Lys
84 65 70 75 80
85
86 TAC AAG ACG CAA AAA GCA ACA ATT CTG GAA GCC TCA TTA AAG AAA TTG 288
87 Tyr Lys Thr Gln Lys Ala Thr Ile Leu Glu Ala Ser Leu Lys Lys Leu
88 85 90 95
89
90 ATT CCT GCT TGG GAA TTT ACA ATT ATT CCT TAC TAT GGA CAA AAA CAT 336
91 Ile Pro Ala Trp Glu Phe Thr Ile Ile Pro Tyr Tyr Gly Gln Lys His
92 100 105 110
93
94 CAA TCT GAT ATC ACT GAT ATT GTA AGT AGT TTG CAA TTA CAG TTC GAA 384
95 Gln Ser Asp Ile Thr Asp Ile Val Ser Ser Leu Gln Leu Gln Phe Glu
96 115 120 125
97
98 TCA TCG GAA GAA GCA GAT AAG GGA AAT AGC CAC AGT AAA AAA ATG CTT 432
99 Ser Ser Glu Glu Ala Asp Lys Gly Asn Ser His Ser Lys Lys Met Leu
100 130 135 140
101
102 AAA GCA CTT CTA AGT GAG GGT GAA AGC ATC TGG GAG ATC ACT GAG AAA 480
103 Lys Ala Leu Leu Ser Glu Gly Glu Ser Ile Trp Glu Ile Thr Glu Lys
104 145 150 155 160
105
106 ATA CTA AAT TCG TTT GAG TAT ACT TCG AGA TTT ACA AAA ACA AAA ACT 528

Patent Application US/07/666,252

107	Ile	Leu	Asn	Ser	Phe	Glu	Tyr	Thr	Ser	Arg	Phe	Thr	Lys	Thr	Lys	Thr	
108					165					170					175		
109																	
110	TTA	TAC	CAA	TTC	CTC	TTC	CTA	GCT	ACT	TTC	ATC	AAT	TGT	GGA	AGA	TTC	576
111	Leu	Tyr	Gln	Phe	Leu	Phe	Leu	Ala	Thr	Phe	Ile	Asn	Cys	Gly	Arg	Phe	
112				180					185					190			
113																	
114	AGC	GAT	ATT	AAG	AAC	GTT	GAT	CCG	AAA	TCA	TTT	AAA	TTA	GTC	CAA	AAT	624
115	Ser	Asp	Ile	Lys	Asn	Val	Asp	Pro	Lys	Ser	Phe	Lys	Leu	Val	Gln	Asn	
116			195					200					205				
117																	
118	AAG	TAT	CTG	GGA	GTA	ATA	ATC	CAG	TGT	TTA	GTG	ACA	GAG	ACA	AAG	ACA	672
119	Lys	Tyr	Leu	Gly	Val	Ile	Ile	Gln	Cys	Leu	Val	Thr	Glu	Thr	Lys	Thr	
120		210					215					220					
121																	
122	AGC	GTT	AGT	AGG	CAC	ATA	TAC	TTC	TTT	AGC	GCA	AGG	GGT	AGG	ATC	GAT	720
123	Ser	Val	Ser	Arg	His	Ile	Tyr	Phe	Phe	Ser	Ala	Arg	Gly	Arg	Ile	Asp	
124	225				230					235						240	
125																	
126	CCA	CTT	GTA	TAT	TTG	GAT	GAA	TTT	TTG	AGG	AAT	TCT	GAA	CCA	GTC	CTA	768
127	Pro	Leu	Val	Tyr	Leu	Asp	Glu	Phe	Leu	Arg	Asn	Ser	Glu	Pro	Val	Leu	
128				245						250					255		
129																	
130	AAA	CGA	GTA	AAT	AGG	ACC	GGC	AAT	TCT	TCA	AGC	AAT	AAA	CAG	GAA	TAC	816
131	Lys	Arg	Val	Asn	Arg	Thr	Gly	Asn	Ser	Ser	Ser	Asn	Lys	Gln	Glu	Tyr	
132				260				265						270			
133																	
134	CAA	TTA	TTA	AAA	GAT	AAC	TTA	GTC	AGA	TCG	TAC	AAT	AAA	GCT	TTG	AAG	864
135	Gln	Leu	Leu	Lys	Asp	Asn	Leu	Val	Arg	Ser	Tyr	Asn	Lys	Ala	Leu	Lys	
136			275					280					285				
137																	
138	AAA	AAT	GCG	CCT	TAT	TCA	ATC	TTT	GCT	ATA	AAA	AAT	GGC	CCA	AAA	TCT	912
139	Lys	Asn	Ala	Pro	Tyr	Ser	Ile	Phe	Ala	Ile	Lys	Asn	Gly	Pro	Lys	Ser	
140		290					295					300					
141																	
142	CAC	ATT	GGA	AGA	CAT	TTG	ATG	ACC	TCA	TTT	CTT	TCA	ATG	AAG	GGC	CTA	960
143	His	Ile	Gly	Arg	His	Leu	Met	Thr	Ser	Phe	Leu	Ser	Met	Lys	Gly	Leu	
144	305					310					315					320	
145																	
146	ACG	GAG	TTG	ACT	AAT	GTT	GTG	GGA	AAT	TGG	AGC	GAT	AAG	CGT	GCT	TCT	1008
147	Thr	Glu	Leu	Thr	Asn	Val	Val	Gly	Asn	Trp	Ser	Asp	Lys	Arg	Ala	Ser	
148					325					330					335		
149																	
150	GCC	GTG	GCC	AGG	ACA	ACG	TAT	ACT	CAT	CAG	ATA	ACA	GCA	ATA	CCT	GAT	1056
151	Ala	Val	Ala	Arg	Thr	Thr	Tyr	Thr	His	Gln	Ile	Thr	Ala	Ile	Pro	Asp	
152				340					345					350			
153																	
154	CAC	TAC	TTC	GCA	CTA	GTT	TCT	CGG	TAC	TAT	GCA	TAT	GAT	CCA	ATA	TCA	1104
155	His	Tyr	Phe	Ala	Leu	Val	Ser	Arg	Tyr	Tyr	Ala	Tyr	Asp	Pro	Ile	Ser	
156			355					360					365				
157																	
158	AAG	GAA	ATG	ATA	GCA	TTG	AAG	GAT	GAG	ACT	AAT	CCA	ATT	GAG	GAG	TGG	1152
159	Lys	Glu	Met	Ile	Ala	Leu	Lys	Asp	Glu	Thr	Asn	Pro	Ile	Glu	Glu	Trp	

Patent Application US/07/666,252

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160          370          375          380
161
162 CAG CAT ATA GAA CAG CTA AAG GGT AGT GCT GAA GGA AGC ATA CGA TAC      1200
163 Gln His Ile Glu Gln Leu Lys Gly Ser Ala Glu Gly Ser Ile Arg Tyr
164 385          390          395          400
165
166 CCC GCA TGG AAT GGG ATA ATA TCA CAG GAG GTA CTA GAC TAC CTT TCA      1248
167 Pro Ala Trp Asn Gly Ile Ile Ser Gln Glu Val Leu Asp Tyr Leu Ser
168          405          410          415
169
170 TCC TAC ATA AAT AGA CGC ATA TAAGTACGCA TTTAAGCATA AACACGCACT      1299
171 Ser Tyr Ile Asn Arg Arg Ile
172          420
173
174 ATGCCGTTCT TCTCATGTAT ATATATATAC AGGCAACACG CAGATATAGG TGCGACGTGA      1359
175
176 ACAGTGAGCT GTATGTGCGC A      1380
177
178
179 (2) INFORMATION FOR SEQ ID NO:2:
180
181 (i) SEQUENCE CHARACTERISTICS:
182 (A) LENGTH: 423 amino acids
183 (B) TYPE: amino acid
184 (D) TOPOLOGY: linear
185
186 (ii) MOLECULE TYPE: protein
187
188 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
189
190 Met Pro Gln Phe Asp Ile Leu Cys Lys Thr Pro Pro Lys Val Leu Val
191 1          5          10          15
192
193 Arg Gln Phe Val Glu Arg Phe Glu Arg Pro Ser Gly Glu Lys Ile Ala
194          20          25          30
195
196 Leu Cys Ala Ala Glu Leu Thr Tyr Leu Cys Trp Met Ile Thr His Asn
197          35          40          45
198
199 Gly Thr Ala Ile Lys Arg Ala Thr Phe Met Ser Tyr Asn Thr Ile Ile
200          50          55          60
201
202 Ser Asn Ser Leu Ser Phe Asp Ile Val Asn Lys Ser Leu Gln Phe Lys
203 65          70          75          80
204
205 Tyr Lys Thr Gln Lys Ala Thr Ile Leu Glu Ala Ser Leu Lys Lys Leu
206          85          90          95
207
208 Ile Pro Ala Trp Glu Phe Thr Ile Ile Pro Tyr Tyr Gly Gln Lys His
209          100          105          110
210
211 Gln Ser Asp Ile Thr Asp Ile Val Ser Ser Leu Gln Leu Gln Phe Glu
212          115          120          125

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Patent Application US/07/666,252

213
214 Ser Ser Glu Glu Ala Asp Lys Gly Asn Ser His Ser Lys Lys Met Leu
215 130 135 140
216
217 Lys Ala Leu Leu Ser Glu Gly Glu Ser Ile Trp Glu Ile Thr Glu Lys
218 145 150 155 160
219
220 Ile Leu Asn Ser Phe Glu Tyr Thr Ser Arg Phe Thr Lys Thr Lys Thr
221 165 170 175
222
223 Leu Tyr Gln Phe Leu Phe Leu Ala Thr Phe Ile Asn Cys Gly Arg Phe
224 180 185 190
225
226 Ser Asp Ile Lys Asn Val Asp Pro Lys Ser Phe Lys Leu Val Gln Asn
227 195 200 205
228
229 Lys Tyr Leu Gly Val Ile Ile Gln Cys Leu Val Thr Glu Thr Lys Thr
230 210 215 220
231
232 Ser Val Ser Arg His Ile Tyr Phe Phe Ser Ala Arg Gly Arg Ile Asp
233 225 230 235 240
234
235 Pro Leu Val Tyr Leu Asp Glu Phe Leu Arg Asn Ser Glu Pro Val Leu
236 245 250 255
237
238 Lys Arg Val Asn Arg Thr Gly Asn Ser Ser Ser Asn Lys Gln Glu Tyr
239 260 265 270
240
241 Gln Leu Leu Lys Asp Asn Leu Val Arg Ser Tyr Asn Lys Ala Leu Lys
242 275 280 285
243
244 Lys Asn Ala Pro Tyr Ser Ile Phe Ala Ile Lys Asn Gly Pro Lys Ser
245 290 295 300
246
247 His Ile Gly Arg His Leu Met Thr Ser Phe Leu Ser Met Lys Gly Leu
248 305 310 315 320
249
250 Thr Glu Leu Thr Asn Val Val Gly Asn Trp Ser Asp Lys Arg Ala Ser
251 325 330 335
252
253 Ala Val Ala Arg Thr Thr Tyr Thr His Gln Ile Thr Ala Ile Pro Asp
254 340 345 350
255
256 His Tyr Phe Ala Leu Val Ser Arg Tyr Tyr Ala Tyr Asp Pro Ile Ser
257 355 360 365
258
259 Lys Glu Met Ile Ala Leu Lys Asp Glu Thr Asn Pro Ile Glu Glu Trp
260 370 375 380
261
262 Gln His Ile Glu Gln Leu Lys Gly Ser Ala Glu Gly Ser Ile Arg Tyr
263 385 390 395 400
264
265 Pro Ala Trp Asn Gly Ile Ile Ser Gln Glu Val Leu Asp Tyr Leu Ser

Patent Application US/07/666,252

266		405		410		415
267						
268	Ser Tyr Ile Asn Arg Arg Ile					
269		420				
270						

PAGE: 1

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/07/666,252

DATE: 04/26/91
TIME: 13:03:31

LINE ERROR

ORIGINAL TEXT

30 Wrong application Serial Number
31 Wrong Filing Date

OK. C (A) APPLICATION NUMBER: US 07/666,252
(B) FILING DATE: 08-MAR-1991

PAGE: 1

SEQUENCE MISSING ITEM REPORT
PATENT APPLICATION US/07/666,252

DATE: 04/26/91
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MANDATORY IDENTIFIER THAT WAS NOT FOUND

PRIOR APPLICATION DATA
APPLICATION NUMBER
FILING DATE

PAGE: 1

SEQUENCE CORRECTION REPORT
PATENT APPLICATION US/07/666,252

DATE: 04/26/91
TIME: 13:03:31

LINE ORIGINAL TEXT

CORRECTED TEXT